WHAT IS CLAIMED IS:

1. A polynucleotide for predicting validity of interferon therapy, comprising a polynucleotide selected from the group consisting of:

(at) the polynucleotide of Sequence ID No. 1 in the sequence listing;

(bt) a modified polynucleotide derived from the polynucleotide (at) by including one or several deletions, substitutions or additions at any positions except for 455th position;

(ct) a polynucleotide containing the sequence which spans from 441st to 455th position of Sequence ID No. 1;

(dt) a polynucleotide containing the sequence which spans from 449the to 459th position of Sequence ID No. 1; and

(et) a complementary strand of the polynucleotide selected from the group consisting of (at), (bt), (ct) and (dt) mentioned above.

2. A polynucleotide for predicting validity of interferon therapy, comprising a polynucleotide selected from the group consisting of:

(ag) the polynucleotide of Sequence ID No. 2 in the sequence listing;

(bg) a modified polynucleotide derived from the polynucleotide (ag) by including one or several deletions, substitutions or additions at any positions

except for 455th position;

(cg) a polynucleotide containing the sequence which spans from 441st to 455th position of Sequence ID No. 2;

(dg) a polynucleotide containing the sequence which spans from 449th to 459th position of Sequence ID No. 2; and

(eg) a complementary strand of the poly nucleotide selected from the group consisting of (ag), (bg), (cg) and (dg) mentioned above.

3. A polynucleotide for predicting validity of interferon therapy, comprising a polynucleotide selected from the group consisting of:

(aa) the polynucleotide of Sequence ID No. 3 in the sequence listing;

(ba) a modified polynucleotide derived from the polynucleotide (aa) by including one or several deletions, substitutions or additions at any positions except for 455th position;

(ca) a polynucleotide containing the sequence which spans from 441st to 455th position of Sequence ID No. 3;

(da) a polynucleotide containing the sequence which spans from 449th to 459th position of Sequence ID No. 3; and

(ea) a complementary strand of the polynucleotide selected from the group consisting of (aa), (ba), (ca)

and (da) mentioned above.

4. A polynucleotide for predicting validity of interferon therapy, comprising a polynucleotide selected from the group consisting of:

(ac) the polynucleotide of Sequence ID No. 4 in the sequence listing;

(bc) a modified polynucleotide derived from the polynucleotide (ac) by including one or several deletions, substitutions or additions at any positions except for 455th position;

(cc) a polynucleotide containing the sequence which spans from 441st to 455th position of Sequence ID No. 4;

(dc) a polynucleotide containing the sequence which spans from 449th to 459th position of Sequence ID No. 4; and

(ec) a complementary strand of the polynucleotide selected from the group consisting of (ac), (bc), (cc) and (dc) mentioned above.

5. A polynucleotide according to any one of claims 1 to 4, further comprising at least one additional polynucleotide connected to said polynucleotide, the additional polynucleotide being selected from the group consisting of a promoter, an enhancer, an upstream activation sequence, a silencers, a upstream suppression sequence, an attenuator, a poly A tail, a nucleus transport signal, Kozak sequence,

ISRE, a drug resistance factor, a gene of signal peptide, a gene of transmembrane domein, a gene of marker protein, a gene of interferon-responding protein, and a gene of interferon-non-responding protein.

6. A method of predicting whether interferon therapy is valid or not for an individual requiring interferon administration, comprising:

1) taking a sample containing a polynucleotide which includes at least one interferon-stimulated response element from the individual; and

2) determining nucleotide located at the 2nd position from the 3' end of said at least one interferon-stimulated response element.

7. The method according to claim 6, further comprising:

3) predicting validity of interferon therapy for said individual, when said nucleotide is thymine.

8. The method according to claim 6, further comprising:

3') predicting that interferon therapy highly possibly invalid for said individual, when said nucleotide is guanine, adenine or cytosine.

9. The method according to claim 6 or 7, wherein said individual is those infected with hepatitis C virus.

10. The method according to any one of claims 6

to 9, wherein said polynucleotide which include at least one interferon-stimulated response element being the polynucleotide according to any one of claims 1 to 4.

11. A test reagent for predicting whether interferon therapy is valid or not for an individual requiring interferon therapy, comprising a polynucleotide according to any one of claims 1 to 4.

12. A probe for detecting polymorphism existing in a promoter region of MxA gene, comprising a polynucleotide according to any one of claims 1 to 4.

13. Use of a polynucleotide according to any one of claims 1 to for predicting validity of interferon.

14. A method for rendering an interferon-insensitive individual to be interferon-sensitive, which comprises introducing polynucleotide according to claim 1 into the interferon-insensitive individual.

15. A vector for rendering an interferon-insensitive individual to be interferon-sensitive, which contains a polynucleotide according to claim 1.

16. Use of a polynucleotide according to claim 1, in the production of pharmaceuticals for rendering an interferon-insensitive individual to be interferon-sensitive.

17. A non-human transgenic animal, which has been introduced with a polynucleotide according to any one of claims 1 to 4.